

10/546000

JC23 Rec'd PCT/PTO 18 AUG 2003

SEQUENCE LISTING

<110> Hamada, Hirofumi
 Ito, Yoshinori
 Takahashi, Kazuhiro
 Morikawa, Masayuki

<120> Methods For Treating Ischemic Diseases

<130> 50026/054001

<150> PCT/JP04/000957

<151> 2004-01-30

<150> JP 2003-040806

<151> 2003-02-19

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3372

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(3372)

<400> 1

atg gac tct tta gcc agc tta gtt ctc tgt gga gtc agc ttg ctc ctt 48
 Met Asp Ser Leu Ala Ser Leu Val Leu Cys Gly Val Ser Leu Leu Leu

1 5 10 15

tct gga act gtg gaa ggt gcc atg gac ttg atc ttg atc aat tcc cta 96
 Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu

20 25 30

cct ctt gta tct gat gct gaa aca tct ctc acc tgc att gcc tct ggg 144
 Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly

35 40 45

tgg cgc ccc cat gag ccc atc acc ata gga agg gac ttt gaa gcc tta 192
 Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu

50 55 60

atg aac cag cac cag gat ccg ctg gaa gtt act caa gat gtg acc aga 240
 Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg

65 70 75 80

gaa tgg gct aaa aaa gtt gtt tgg aag aga gaa aag gct agt aag atc 288
 Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile

85 90 95

aat ggt gct tat ttc tgt gaa ggg cga gtt cga gga gag gca atc agg	336
Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg	
100 105 110	
ata cga acc atg aag atg cgt caa caa gct tcc ttc cta cca gct act	384
Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr	
115 120 125	
tta act atg act gtg gac aag gga gat aac gtg aac ata tct ttc aaa	432
Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys	
130 135 140	
aag gta ttg att aaa gaa gaa gat gca gtg att tac aaa aat ggt tcc	480
Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser	
145 150 155 160	
ttc atc cat tca gtg ccc cgg cat gaa gta cct gat att cta gaa gta	528
Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val	
165 170 175	
cac ctg cct cat gct cag ccc cag gat gct gga gtg tac tcg gcc agg	576
His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg	
180 185 190	
tat ata gga gga aac ctc ttc acc tcg gcc ttc acc agg ctg ata gtc	624
Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val	
195 200 205	
cgg aga tgt gaa gcc cag aag tgg gga cct gaa tgc aac cat ctc tgt	672
Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys	
210 215 220	
act gct tgt atg aac aat ggt gtc tgc cat gaa gat act gga gaa tgc	720
Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys	
225 230 235 240	
att tgc cct cdt ggg ttt atg gga agg acg tgt gag aag gct tgt gaa	768
Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu	
245 250 255	
ctg cac acg ttt ggc aga act tgt aaa gaa agg tgc agt gga caa gag	816
Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu	
260 265 270	
gga tgc aag tct tat gtg ttc tgt ctc cct gac ccc tat ggg tgt tcc	864
Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser	
275 280 285	
tgt gcc aca ggc tgg aag ggt ctg cag tgc aat gaa gca tgc cac cct	912
Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro	
290 295 300	
ggg ttt tac ggg cca gat tgt aag ctt agg tgc agc tgc aac aat ggg	960
Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly	
305 310 315 320	
gag atg tgt gat cgc ttc caa gga tgt ctc tgc tct cca gga tgg cag	1008

Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln	325	330	335	
ggg ctc cag tgt gag aga gaa ggc ata ccg agg atg acc cca aag ata				1056
Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile	340	345	350	
gtg gat ttg cca gat cat ata gaa gta aac agt ggt aaa ttt aat ccc				1104
Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro	355	360	365	
att tgc aaa gct tct ggc tgg ccg cta cct act aat gaa gaa atg acc				1152
Ile Cys Lys Ala Ser Gly Trp Pro Leu Pro Thr Asn Glu Glu Met Thr	370	375	380	
ctg gtg aag ccg gat ggg aca gtg ctc cat cca aaa gac ttt aac cat				1200
Leu Val Lys Pro Asp Gly Thr Val Leu His Pro Lys Asp Phe Asn His	385	390	395	400
acg gat cat ttc tca gta gcc ata ttc acc atc cac cgg atc ctc ccc				1248
Thr Asp His Phe Ser Val Ala Ile Phe Thr Ile His Arg Ile Leu Pro	405	410	415	
cct gac tca gga gtt tgg gtc tgc agt gtg aac aca gtg gct ggg atg				1296
Pro Asp Ser Gly Val Trp Val Cys Ser Val Asn Thr Val Ala Gly Met	420	425	430	
gtg gaa aag ccc ttc aac att tct gtt aaa gtt ctt cca aag ccc ctg				1344
Val Glu Lys Pro Phe Asn Ile Ser Val Lys Val Leu Pro Lys Pro Leu	435	440	445	
aat gcc cca aac gtg att gac act gga cat aac ttt gct gtc atc aac				1392
Asn Ala Pro Asn Val Ile Asp Thr Gly His Asn Phe Ala Val Ile Asn	450	455	460	
atc agc tct gag cct tac ttt ggg gat gga cca atc aaa tcc aag aag				1440
Ile Ser Ser Glu Pro Tyr Phe Gly Asp Gly Pro Ile Lys Ser Lys Lys	465	470	475	480
ctt cta tac aaa ccc gtt aat cac tat gag gct tgg caa cat att caa				1488
Leu Leu Tyr Lys Pro Val Asn His Tyr Glu Ala Trp Gln His Ile Gln	485	490	495	
gtg aca aat gag att gtt aca ctc aac tat ttg gaa cct cgg aca gaa				1536
Val Thr Asn Glu Ile Val Thr Leu Asn Tyr Leu Glu Pro Arg Thr Glu	500	505	510	
tat gaa ctc tgt gtg caa ctg gtc cgt cgt gga gag ggt ggg gaa ggg				1584
Tyr Glu Leu Cys Val Gln Leu Val Arg Arg Gly Glu Gly Gly Glu Gly	515	520	525	
cat cct gga cct gtg aga cgc ttc aca aca gct tct atc gga ctc cct				1632
His Pro Gly Pro Val Arg Arg Phe Thr Thr Ala Ser Ile Gly Leu Pro	530	535	540	
cct cca aga ggt cta aat ctc ctg cct aaa agt cag acc act cta aat				1680
Pro Pro Arg Gly Leu Asn Leu Leu Pro Lys Ser Gln Thr Thr Leu Asn				

545	550	555	560	
ttg acc tgg caa cca ata ttt cca agc tcg gaa gat gac ttt tat gtt				1728
Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val	565	570	575	
gaa gtg gag aga agg tct gtg caa aaa agt gat cag cag aat att aaa				1776
Glu Val Glu Arg Arg Ser Val Gln Lys Ser Asp Gln Gln Asn Ile Lys	580	585	590	
gtt cca ggc aac ttg act tcg gtg cta ctt aac aac tta cat ccc agg				1824
Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg	595	600	605	
gag cag tac gtg gtc cga gct aga gtc aac acc aag gcc cag ggg gaa				1872
Glu Gln Tyr Val Val Arg Ala Arg Val Asn Thr Lys Ala Gln Gly Glu	610	615	620	
ttg agt gaa gat ctc act gct tgg acc ctt agt gac att ctt cct cct				1920
Trp Ser Glu Asp Leu Thr Ala Trp Thr Leu Ser Asp Ile Leu Pro Pro	625	630	635, 640	
caa cca gaa aac atc aag att tcc aac att aca cac tcc tcg gct gtg				1968
Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val	645	650	655	
att tct tgg aca ata ttg gat ggc tat tct att tct tct att act atc				2016
Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile	660	665	670	
cgt tac aag gtt caa ggc aag aat gaa gac cag cac gtt gat gtg aag				2064
Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys	675	680	685	
ata aag aat gcc acc atc att cag tat cag ctc aag ggc cta gag cct				2112
Ile Lys Asn Ala Thr Ile Ile Gln Tyr Gln Leu Lys Gly Leu Glu Pro	690	695	700	
gaa aca gca tac cag gtg gac att ttt gca gag aac aac ata ggg tca				2160
Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser	705	710	715 720	
agc aac cca gcc ttt tct cat gaa ctg gtg acc ctc cca gaa tct caa				2208
Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln	725	730	735	
gca cca gcg gac ctc gga ggg ggg aag atg ctg ctt ata gcc atc ctt				2256
Ala Pro Ala Asp Leu Gly Gly Gly Lys Met Leu Leu Ile Ala Ile Leu	740	745	750	
ggc tct gct gga atg acc tgc ctg act gtg ctg ttg gcc ttt ctg atc				2304
Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile	755	760	765	
ata ttg caa ttg aag agg gca aat gtg caa agg aga atg gcc caa gcc				2352
Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala	770	775	780	

ttc caa aac gtg agg gaa gaa cca gct gtg cag ttc aac tca ggg act	2400
Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr	
785 790 795 800	
ctg gcc cta aac agg aag gtc aaa aac aac cca gat cct aca att tat	2448
Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr	
805 810 815	
cca gtg ctt gac tgg aat gac atc aaa ttt caa gat gtg att ggg gag	2496
Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu	
820 825 830	
ggc aat ttt ggc caa gtt ctt aag gcg cgc atc aag aag gat ggg tta	2544
Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu	
835 840 845	
cgg atg gat gct gcc atc aaa aga atg aaa gaa tat gcc tcc aaa gat	2592
Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp	
850 855 860	
gat cac agg gac ttt gca gga gaa ctg gaa gtt ctt tgt aaa ctt gga	2640
Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly	
865 870 875 880	
cac cat cca aac atc atc aat ctc tta gga gca tgt gaa cat cga ggc	2688
His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly	
885 890 895	
tac ttg tac ctg gcc att gag tac gcg ccc cat gga aac ctt ctg gac	2736
Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp	
900 905 910	
ttc ctt cgc aag agc cgt gtg ctg gag acg gac cca gca ttt gcc att	2784
Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile	
915 920 925	
gcc aat agc acc gcg tcc aca ctg tcc tcc cag cag ctc ctt cac ttc	2832
Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe	
930 935 940	
gct gcc gac gtg gcc cgg ggc atg gac tac ttg agc caa aaa cag ttt	2880
Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe	
945 950 955 960	
atc cac agg gat ctg gct gcc aga aac att tta gtt ggt gaa aac tat	2928
Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr	
965 970 975	
gtg gca aaa ata gca gat ttt gga ttg tcc cga ggt caa gag gtg tac	2976
Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr	
980 985 990	
gtg aaa aag aca atg gga agg ctc cca gtg cgc tgg atg gcc atc gag	3024
Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu	
995 1000 1005	

tca ctg aat tac agt gtg tac aca acc aac agt gat gta tgg tcc tat	3072
Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser Tyr	
1010 1015 1020	
ggt gtg tta cta tgg gag att gtt agc tta gga ggc aca ccc tac tgc	3120
Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro Tyr Cys	
1025 1030 1035 1040	
ggg atg act tgt gca gaa ctc tac gag aag ctg ccc cag ggc tac aga	3168
Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln Gly Tyr Arg	
1045 1050 1055	
ctg gag aag ccc ctg aac tgt gat gat gag gtg tat gat cta atg aga	3216
Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr Asp Leu Met Arg	
1060 1065 1070	
caa tgc tgg cgg gag aag cct tat gag agg cca tca ttt gcc cag ata	3264
Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro Ser Phe Ala Gln Ile	
1075 1080 1085	
ttg gtg tcc tta aac aga atg tta gag gag cga aag acc tac gtg aat	3312
Leu Val Ser Leu Asn Arg Met Leu Glu Glu Arg Lys Thr Tyr Val Asn	
1090 1095 1100	
acc acg ctt tat gag aag ttt act tat gca gga att gac tgt tct gct	3360
Thr Thr Leu Tyr Glu Lys Phe Thr Tyr Ala Gly Ile Asp Cys Ser Ala	
1105 1110 1115 1120	
gaa gaa gcg gcc	3372
Glu Glu Ala Ala	

<210> 2
 <211> 1124
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Asp Ser Leu Ala Ser Leu Val Leu Cys Gly Val Ser Leu Leu Leu	
1 5 10 15	
Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu	
20 25 30	
Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly	
35 40 45	
Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu	
50 55 60	
Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg	
65 70 75 80	
Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile	
85 90 95	
Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg	
100 105 110	
Ile Arg Thr Met Lys Met Arg Gln Ala Ser Phe Leu Pro Ala Thr	
115 120 125	
Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys	
130 135 140	

Lys	Val	Leu	Ile	Lys	Glu	Glu	Asp	Ala	Val	Ile	Tyr	Lys	Asn	Gly	Ser	145	150	155	160
Phe	Ile	His	Ser	Val	Pro	Arg	His	Glu	Val	Pro	Asp	Ile	Leu	Glu	Val	165	170	175	
His	Leu	Pro	His	Ala	Gln	Pro	Gln	Asp	Ala	Gly	Val	Tyr	Ser	Ala	Arg	180	185	190	
Tyr	Ile	Gly	Gly	Asn	Leu	Phe	Thr	Ser	Ala	Phe	Thr	Arg	Leu	Ile	Val	195	200	205	
Arg	Arg	Cys	Glu	Ala	Gln	Lys	Trp	Gly	Pro	Glu	Cys	Asn	His	Leu	Cys	210	215	220	
Thr	Ala	Cys	Met	Asn	Asn	Gly	Val	Cys	His	Glu	Asp	Thr	Gly	Glu	Cys	225	230	235	240
Ile	Cys	Pro	Pro	Gly	Phe	Met	Gly	Arg	Thr	Cys	Glu	Lys	Ala	Cys	Glu	245	250	255	
Leu	His	Thr	Phe	Gly	Arg	Thr	Cys	Lys	Glu	Arg	Cys	Ser	Gly	Gln	Glu	260	265	270	
Gly	Cys	Lys	Ser	Tyr	Val	Phe	Cys	Leu	Pro	Asp	Pro	Tyr	Gly	Cys	Ser	275	280	285	
Cys	Ala	Thr	Gly	Trp	Lys	Gly	Leu	Gln	Cys	Asn	Glu	Ala	Cys	His	Pro	290	295	300	
Gly	Phe	Tyr	Gly	Pro	Asp	Cys	Lys	Leu	Arg	Cys	Ser	Cys	Asn	Asn	Gly	305	310	315	320
Glu	Met	Cys	Asp	Arg	Phe	Gln	Gly	Cys	Leu	Cys	Ser	Pro	Gly	Trp	Gln	325	330	335	
Gly	Leu	Gln	Cys	Glu	Arg	Glu	Gly	Ile	Pro	Arg	Met	Thr	Pro	Lys	Ile	340	345	350	
Val	Asp	Leu	Pro	Asp	His	Ile	Glu	Val	Asn	Ser	Gly	Lys	Phe	Asn	Pro	355	360	365	
Ile	Cys	Lys	Ala	Ser	Gly	Trp	Pro	Leu	Pro	Thr	Asn	Glu	Glu	Met	Thr	370	375	380	
Leu	Val	Lys	Pro	Asp	Gly	Thr	Val	Leu	His	Pro	Lys	Asp	Phe	Asn	His	385	390	395	400
Thr	Asp	His	Phe	Ser	Val	Ala	Ile	Phe	Thr	Ile	His	Arg	Ile	Leu	Pro	405	410	415	
Pro	Asp	Ser	Gly	Val	Trp	Val	Cys	Ser	Val	Asn	Thr	Val	Ala	Gly	Met	420	425	430	
Val	Glu	Lys	Pro	Phe	Asn	Ile	Ser	Val	Lys	Val	Leu	Pro	Lys	Pro	Leu	435	440	445	
Asn	Ala	Pro	Asn	Val	Ile	Asp	Thr	Gly	His	Asn	Phe	Ala	Val	Ile	Asn	450	455	460	
Ile	Ser	Ser	Glu	Pro	Tyr	Phe	Gly	Asp	Gly	Pro	Ile	Lys	Ser	Lys	Lys	465	470	475	480
Leu	Leu	Tyr	Lys	Pro	Val	Asn	His	Tyr	Glu	Ala	Trp	Gln	His	Ile	Gln	485	490	495	
Val	Thr	Asn	Glu	Ile	Val	Thr	Leu	Asn	Tyr	Leu	Glu	Pro	Arg	Thr	Glu	500	505	510	
Tyr	Glu	Leu	Cys	Val	Gln	Leu	Val	Arg	Arg	Gly	Glu	Gly	Gly	Glu	Gly	515	520	525	
His	Pro	Gly	Pro	Val	Arg	Arg	Phe	Thr	Thr	Ala	Ser	Ile	Gly	Leu	Pro	530	535	540	
Pro	Pro	Arg	Gly	Leu	Asn	Leu	Leu	Pro	Lys	Ser	Gln	Thr	Thr	Leu	Asn	545	550	555	560
Leu	Thr	Trp	Gln	Pro	Ile	Phe	Pro	Ser	Ser	Glu	Asp	Asp	Phe	Tyr	Val	565	570	575	
Glu	Val	Glu	Arg	Ser	Val	Gln	Lys	Ser	Asp	Gln	Gln	Asn	Ile	Lys		580	585	590	
Val	Pro	Gly	Asn	Leu	Thr	Ser	Val	Leu	Leu	Asn	Asn	Leu	His	Pro	Arg				

Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr Asp Leu Met Arg
 1060 1065 1070
 Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro Ser Phe Ala Gln Ile
 1075 1080 1085
 Leu Val Ser Leu Asn Arg Met Leu Glu Glu Arg Lys Thr Tyr Val Asn
 1090 1095 1100
 Thr Thr Leu Tyr Glu Lys Phe Thr Tyr Ala Gly Ile Asp Cys Ser Ala
 1105 1110 1115 1120
 Glu Glu Ala Ala

<210> 3
 <211> 1494
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1494)

<400> 3
 atg aca gtt ttc ctt tcc ttt gct ttc ctc gct gcc att ctg act cac 48
 Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
 1 5 10 15
 ata ggg tgc agc aat cag cgc cga agt cca gaa aac agt ggg aga aga 96
 Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
 20 25 30
 tat aac cgg att caa cat ggg caa tgt gcc tac act ttc att ctt cca 144
 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
 35 40 45
 gaa cac gat ggc aac tgt cgt gag agt acg aca gac cag tac aac aca 192
 Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
 50 55 60
 aac gct ctg cag aga gat gct cca cac gtg gaa ccg gat ttc tct tcc 240
 Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
 65 70 75 80
 cag aaa ctt caa cat ctg gaa cat gtg atg gaa aat tat act cag tgg 288
 Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
 85 90 95
 ctg caa aaa ctt gag aat tac att gtg gaa aac atg aag tcg gag atg 336
 Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
 100 105 110
 gcc cag ata cag cag aat gca gtt cag aac cac acg gct acc atg ctg 384
 Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
 115 120 125
 gag ata gga acc agc ctc ctc tct cag act gca gag cag acc aga aag 432
 Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
 130 135 140

ctg aca gat gtt gag acc cag gta cta aat caa act tct cga ctt gag	480
Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu	
145 150 155 160	
ata cag ctg ctg gag aat tca tta tcc acc tac aag cta gag aag caa	528
Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln	
165 170 175	
ctt ctt caa cag aca aat gaa atc ttg aag atc cat gaa aaa aac agt	576
Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser	
180 185 190	
tta tta gaa cat aaa atc tta gaa atg gaa gga aaa cac aag gaa gag	624
Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu	
195 200 205	
ttg gac acc tta aag gaa gag aaa gag aac ctt caa ggc ttg gtt act	672
Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr	
210 215 220	
cgt caa aca tat ata atc cag gag ctg gaa aag caa tta aac aga gct	720
Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala	
225 230 235 240	
acc acc aac aac agt gtc ctt cag aag cag caa ctg gag ctg atg gac	768
Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp	
245 250 255	
aca gtc cac aac ctt gtc aat ctt tgc act aaa gaa ggt gtt tta cta	816
Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu	
260 265 270	
aag gga gga aaa aga gag gaa gag aaa cca ttt aga gac tgt gca gat	864
Lys Gly Gly Lys Arg Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp	
275 280 285	
gta tat caa gct ggt ttt aat aaa agt gga atc tac act att tat att	912
Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile	
290 295 300	
aat aat atg cca gaa ccc aaa aag gtg ttt tgc aat atg gat gtc aat	960
Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn	
305 310 315 320	
ggg gga ggt tgg act gta ata caa cat cgt gaa gat gga agt cta gat	1008
Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp	
325 330 335	
ttc caa aga ggc tgg aag gaa tat aaa atg ggt ttt gga aat ccc tcc	1056
Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser	
340 345 350	
ggt gaa tat tgg ctg ggg aat gag ttt att ttt gcc att acc agt cag	1104
Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln	
355 360 365	

agg cag tac atg cta aga att gag tta atg gac tgg gaa ggg aac cga 1152
 Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
 370 375 380

gcc tat tca cag tat gac aga ttc cac ata gga aat gaa aag caa aac 1200
 Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
 385 390 395 400

tat agg ttg tat tta aaa ggt cac act ggg aca gca gga aaa cag agc 1248
 Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
 405 410 415

agc ctg atc tta cac ggt gct gat ttc agc act aaa gat gct gat aat 1296
 Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
 420 425 430

gac aac tgt atg tgc aaa tgt gcc ctc atg tta aca gga gga tgg tgg 1344
 Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
 435 440 445

ttt gat gct tgt ggc ccc tcc aat cta aat gga atg ttc tat act gcg 1392
 Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
 450 455 460

gga caa aac cat gga aaa ctg aat ggg ata aag tgg cac tac ttc aaa 1440
 Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
 465 470 475 480

ggg ccc agt tac tcc tta cgt tcc aca act atg atg att cga cct tta 1488
 Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu
 485 490 495

gat ttt 1494
 Asp Phe

<210> 4
 <211> 498
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
 1 5 10 15
 Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
 20 25 30
 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
 35 40 45
 Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
 50 55 60
 Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
 65 70 75 80
 Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
 85 90 95
 Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
 100 105 110

<220>

<223> Artificially synthesized sequence

<400> 5

```
actagttatt aatagtaatc aattacgggg tcattagttc atagcccata tatggagttc 60
cgcgttacat aacttacggt aaatggcccc cctggctgac cgcccaacga ccccgccca 120
ttgacgtcaa taatgacgta tgttcccata gtaacgccaa tagggacttt ccattgacgt 180
caatgggtgg agtattttacg gtaaaactgcc cacttggcag tacatcaagt gtatcatatg 240
ccaagtacgc cccctattga cgtcaatgac ggtaaatggc ccgcctggca ttatgcccag 300
tacatgacct tatgggactt tcctacttgg cagtacatct acgtattagt catcgctatt 360
accatggtcg aggtgagccc cacgttctgc ttcactctcc ccatctcccc cccctcccca 420
cccccaattt tgtattttatt tatttttttaa ttattttgtg cagcgatggg ggcggggggg 480
gggggggggg gcgcgccagg cggggcgggg cggggcgagg ggcggggcgg ggcgaggcgg 540
agaggtgcgg cggcagccaa tcagagcggc gcgctccgaa agtttccctt tatggcgagg 600
cggcggcggc ggcggcccta taaaaagcga agcgcgcggc gggcggggag tcgctgcgac 660
gctgccttcg ccccgctgcc cgctccgccg ccgcctcgcg ccgcccgcgc cggctctgac 720
tgaccgcggt actcccacag gtgagcgggc gggacggccc ttctcctcgg ggctgtaatt 780
agcgcttggt ttaatgacgg cttgtttctt ttctgtggct gcgtgaaagc cttgaggggc 840
tccgggaggg ccctttgtgc ggggggagcg gctcgggggg tgcgtgcgtg tgtgtgtgcg 900
tggggagcgc cgcgtgcggc tccgcgctgc ccggcggtg tgagcgctgc gggcgcgggc 960
cggggctttg tgcgtccgc agtgtgcgc aggggagcgc ggcggggggc ggtgccccgc 1020
ggtgcggggg gggctgcgag gggaacaaag gctgcgtgcg ggggtgtgtc gtgggggggt 1080
gagcaggggg tgtgggcgcg tcggtcgggc tgcaaccccc cctgcacccc cctccccgag 1140
ttgctgagca cggcccggct tcgggtgcgg ggctccgtac ggggcgtggc gcggggctcg 1200
ccgtgcgggg cgggggggtg cggcaggtgg ggggtgccgg cggggcgggg ccgcctcggg 1260
ccggggaggg ctcgggggag gggcgcgggc gcccccgag ccgcggcggc tgcgaggcg 1320
cggcgagccg cagccattgc cttttatggt aatcgtgcga gagggcgcag ggacttcctt 1380
tgtcccaaat ctgtgcggag ccgaaatctg ggaggcgccg ccgcaccccc tctagcgggc 1440
gcggggcgaa gcggtgcggc gccggcagga aggaaatggg cggggagggc cttcgtgcgt 1500
cgccgcgcgc ccgtccctt ctccctctcc agcctcgggg ctgtccgcgg ggggacggct 1560
gccttcgggg gggacggggc agggcggggg tcggcttctg gcgtgtgacc ggcggctcta 1620
gagcctctgc taaccatgtt catgccttct tctttttcct acagctcctg ggcaacgtgc 1680
tggttattgt gctgtctcat cattttggca aagaattcgg cttgatcgaa gcttgcccac 1740
catg
```

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> an artificially synthesized primer

<400> 6

cagaggcagt acatgctaag aattgagtta

30

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> an artificially synthesized primer

<400> 7

agatgctcaa ggggcttcat gatg

24

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> an artificially synthesized primer

<400> 8
tattgggagc ctggtcacca

20

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> an artificially synthesized primer

<400> 9
ccaccttctt gatgtcatca

20